

SEQUENCE LISTING

<110> Ajinomoto Co., Inc.

<120> GENES INVOLVED IN POLYSACCHARIDE PRODUCTION AND
UTILIZATION THEREOF

<130> US-107

<150> JP 2003-32075

<151> 2003-02-10

<160> 13

<170> PatentIn Ver. 2.0

<210> 1

<211> 1404

<212> DNA

<213> *Methylophilus methylotrophus*

<220>

<221> CDS

<222> (1).. (1404)

<400> 1

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Gly Ser Asn Pro Leu Tyr Met Leu Glu Ser Leu Val Glu Pro Leu Val
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atg gtg ttt gtg ctg tgg ggg ttg ttt att tat acc gaa aac cgc att 144
Met Val Phe Val Leu Trp Gly Leu Phe Ile Tyr Thr Glu Asn Arg Ile
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ccg atg tog att ttt att aca tcg ata gtg ctg ttt tog att tct ttc 192

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Pro Ser Gly Ala Lys Ile Arg Lys Gly Phe Ala Lys Met Cys Arg Asp	
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gtg att ggt caa tgg ctg gtc att gcc acc ttt ttg ctg acc ttt gct	288
Val Ile Gly Gln Trp Leu Val Ile Ala Thr Phe Leu Leu Thr Phe Ala	
85 90 95	
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Tyr Ile Thr Arg Tyr Ile Thr Leu Tyr Ser Glu Lys Leu Ile Leu Ala	
100 105 110	
tgg ttg att gtg acg cca gtt gcc cag att att gcg ttg cag tta cta	384
Trp Leu Ile Val Thr Pro Val Ala Gln Ile Ile Ala Leu Gln Leu Leu	
115 120 125	
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Lys Trp Ala Ser Pro Lys Leu Ile Glu Trp Gln Gly Pro Arg Gln Asn	
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165 170 175	
gac cgc gcg cct aac cgg ctt ccg cac ata gat tct tat ccg gta ctt	576
Asp Arg Ala Pro Asn Arg Leu Pro His Ile Asp Ser Tyr Pro Val Leu	
180 185 190	
ggc agc ttg aat gaa ctg agt cat tac ctg aaa tca cac act gta cac	624
Gly Ser Leu Asn Glu Leu Ser His Tyr Leu Lys Ser His Thr Val His	
195 200 205	
aaa ctt tat atc gct tta ccg atg tcc agt cac cct cgt att ttg aaa	672
Lys Leu Tyr Ile Ala Leu Pro Met Ser Ser His Pro Arg Ile Leu Lys	
210 215 220	
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Leu Leu Asp Asp Leu Lys Asp Thr Thr Ala Ser Ile Tyr Phe Val Pro	
225 230 235 240	
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260 265 270	
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Gly Phe Ile Lys Arg Thr Ala Asp Ile Leu Phe Ser Leu Leu Val Leu	
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Ile Leu Ile Ser Pro Ile Leu Ile Gly Ile Ala Ile Ala Val Lys Leu	
290 295 300	
acc tct cct ggc ccc gtt att ttc aag caa cgt cgt tac ggc ttg gat	960
Thr Ser Pro Gly Pro Val Ile Phe Lys Gln Arg Arg Tyr Gly Leu Asp	
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Gly Gln Gln Ile Leu Val Tyr Lys Phe Arg Ser Met Thr Val Thr Glu	
325 330 335	
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His Ala Val Ala His Asn Glu Glu Tyr Arg Lys Leu Ile Lys Gly Tyr	
385 390 395 400	
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<212> PRT

<213> *Methylophilus methylotrophus*

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Val Ile Gly Gln Trp Leu Val Ile Ala Thr Phe Leu Leu Thr Phe Ala
85 90 95
Tyr Ile Thr Arg Tyr Ile Thr Leu Tyr Ser Glu Lys Leu Ile Leu Ala
100 105 110
Trp Leu Ile Val Thr Pro Val Ala Gln Ile Ile Ala Leu Gln Leu Leu
115 120 125
Lys Trp Ala Ser Pro Lys Leu Ile Glu Trp Gln Gly Pro Arg Gln Asn
130 135 140

Thr Leu Ile Ile Gly Leu Asn Glu Gln Gly Leu Leu Leu Ala Asp Asn
145 150 155 160

Leu Lys Arg Asp Tyr Tyr Gln Arg Ile Asn Ile Leu Gly Phe Phe Glu			
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Asp Arg Ala Pro Asn Arg Leu Pro His Ile Asp Ser Tyr Pro Val Leu			
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Gly Ser Leu Asn Glu Leu Ser His Tyr Leu Lys Ser His Thr Val His			
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Lys Leu Tyr Ile Ala Leu Pro Met Ser Ser His Pro Arg Ile Leu Lys			
	210	215	220
Leu Leu Asp Asp Leu Lys Asp Thr Thr Ala Ser Ile Tyr Phe Val Pro			
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Asp Ile Phe Val Thr Asp Leu Ile Gln Gly Arg Val Ser Asp Val Asn			
	245	250	255
Gly Ile Pro Val Val Ser Val Cys Asp Thr Pro Phe Thr Gly Met Asp			
	260	265	270
Gly Phe Ile Lys Arg Thr Ala Asp Ile Leu Phe Ser Leu Leu Val Leu			
	275	280	285
Ile Leu Ile Ser Pro Ile Leu Ile Gly Ile Ala Ile Ala Val Lys Leu			
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Thr Ser Pro Gly Pro Val Ile Phe Lys Gln Arg Arg Tyr Gly Leu Asp			
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Gly Gln Gln Ile Leu Val Tyr Lys Phe Arg Ser Met Thr Val Thr Glu			
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Asp Gly Ala Thr Val Thr Gln Ala Thr Arg Asn Asp Gln Arg Ile Thr			
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Pro Leu Gly Ala Phe Leu Arg Lys Thr Ser Leu Asp Glu Leu Pro Gln			
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Met Val Arg His Lys Val Lys Pro Gly Ile Thr Gly Trp Ala Gln Val			
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Asn Gly Phe Arg Gly Glu Thr Asp Thr Leu Glu Lys Met Glu Gln Arg			
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Val His Tyr Asp Leu Glu Tyr Leu Arg Asn Trp Ser Pro Arg Leu Asp			
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Gly Ala Tyr
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<211> 1422

<212> DNA

<213> *Methylophilus methylotrophus*

<220>

<221> CDS

<222> (1)..(1422)

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His Arg Phe Leu Val Ala Glu Gln Leu Arg Gln Val Asn Leu Thr Pro	
65 70 75 80	
gag gcg att gtg ctg gag ccg gtg gcg cga aat acg gca cct gcg att	288
Glu Ala Ile Val Leu Glu Pro Val Ala Arg Asn Thr Ala Pro Ala Ile	
85 90 95	
gct gct gcg gct gtg act tta aaa gac aaa gat gtc ttg atg ctg gtg	336
Ala Ala Ala Ala Val Thr Leu Lys Asp Lys Asp Val Leu Met Leu Val	

100	105	110	
ttg cct gcg gat cat gtg att act gac gtc act gct ttt gag gct gct	384		
Leu Pro Ala Asp His Val Ile Thr Asp Val Thr Ala Phe Glu Ala Ala			
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gtg cgt cgt gcc tgc gtt gca gca gag cag ggg aaa ctg gtc aca ttt	432		
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130	135	140	
ggg ata gag cct aca cag ccg gaa acc ggt tat ggt tat atc caa tca	480		
Gly Ile Glu Pro Thr Gln Pro Glu Thr Gly Tyr Gly Tyr Ile Gln Ser			
145	150	155	160
ggg gca gaa ttg gaa gca tgt gat ggt tgc ttt gaa gtg gca cgt ttt	528		
Gly Ala Glu Leu Glu Ala Cys Asp Gly Cys Phe Glu Val Ala Arg Phe			
165	170	175	
gtt gag aag cct gat gct gcg act gca cag caa tat ttg gat gcc gga	576		
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180	185	190	
aac ttt tat tgg aac agc ggc atg ttt ttg ttt aaa ccg gct gtg ttc	624		
Asn Phe Tyr Trp Asn Ser Gly Met Phe Leu Phe Lys Pro Ala Val Phe			
195	200	205	
ctg gct gag ttg cag caa tac gcg cca gcc atg gtc agt gcg gta agc	672		
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210	215	220	
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225	230	235	240
gag gcc tcg ttt gct gag tct cct tct gat tca att gac tat gcc gtc	768		
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245	250	255	
atg gaa aaa acc aaa ctg gcg gcc gtg gta cct gcc agc atg ggg tgg	816		
Met Glu Lys Thr Lys Leu Ala Ala Val Val Pro Ala Ser Met Gly Trp			
260	265	270	
aat gat gtt ggc tca tgg act gcc tta aaa gaa gtg cag ccc aat gat	864		
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275	280	285	
gcg gat ggg aat gct aca cgc ggg gat gtg ttt ctt aaa aat gtg aaa	912		
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gag gat ttg ctg att gtt gaa acc agt gat gcg atc ctg gtt gcg cac			1008
Glu Asp Leu Leu Ile Val Glu Thr Ser Asp Ala Ile Leu Val Ala His			
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340	345	350	
agc gga cgt tct gaa cat aag atg cat ccc cgt gtt tat cgc cct tgg			1104
Ser Gly Arg Ser Glu His Lys Met His Pro Arg Val Tyr Arg Pro Trp			
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ggt tgg tac gag gga atc gat atc ggc gag cgt ttc cag gtc aag cgt			1152
Gly Trp Tyr Glu Gly Ile Asp Ile Gly Glu Arg Phe Gln Val Lys Arg			
370	375	380	
att atg gtg aaa cca ggt gaa aga ttg tca ctg caa atg cat cat cat			1200
Ile Met Val Lys Pro Gly Glu Arg Leu Ser Leu Gln Met His His His			
385	390	395	400
cgg gct gag cac tgg gtg gtt gtc agt ggg tct gcc atg atc act att			1248
Arg Ala Glu His Trp Val Val Val Ser Gly Ser Ala Met Ile Thr Ile			
405	410	415	
gat gat gtc acc aag ctc tat act gaa aac gaa tct act tat ata ccg			1296
Asp Asp Val Thr Lys Leu Tyr Thr Glu Asn Glu Ser Thr Tyr Ile Pro			
420	425	430	
att ggc tca acg cac cga cta gag aat cca ggt aaa ttg cct ttg cat			1344
Ile Gly Ser Thr His Arg Leu Glu Asn Pro Gly Lys Leu Pro Leu His			
435	440	445	
tta atc gag gtg caa tcc ggt agt tat ctt gga gaa gat gac atc gtg			1392
Leu Ile Glu Val Gln Ser Gly Ser Tyr Leu Gly Glu Asp Asp Ile Val			
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<212> PRT

<213> *Methylophilus methylotrophus*

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Pro	Leu	Val	Thr	Glu	Asn	Thr	Met	Leu	Gln	Glu	Thr	Leu	Ile	Arg	Leu
				35				40					45		
Ser	Ser	Trp	Ala	Asp	Val	Gly	His	Pro	Ile	Val	Val	Cys	Gly	Asn	Asp
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His	Arg	Phe	Leu	Val	Ala	Glu	Gln	Leu	Arg	Gln	Val	Asn	Leu	Thr	Pro
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Glu	Ala	Ile	Val	Leu	Glu	Pro	Val	Ala	Arg	Asn	Thr	Ala	Pro	Ala	Ile
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Ala	Ala	Ala	Ala	Val	Thr	Leu	Lys	Asp	Lys	Asp	Val	Leu	Met	Leu	Val
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Leu	Pro	Ala	Asp	His	Val	Ile	Thr	Asp	Val	Thr	Ala	Phe	Glu	Ala	Ala
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Val	Glu	Lys	Pro	Asp	Ala	Ala	Thr	Ala	Gln	Gln	Tyr	Leu	Asp	Ala	Gly
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Leu	Ala	Glu	Leu	Gln	Gln	Tyr	Ala	Pro	Ala	Met	Val	Ser	Ala	Val	Ser
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Asn	Ala	Val	Ala	Gln	Ser	Tyr	Lys	Asp	Leu	Asp	Phe	Val	Arg	Leu	His
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Ala	Asp	Gly	Asn	Ala	Thr	Arg	Gly	Asp	Val	Phe	Leu	Lys	Asn	Val	Lys
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Arg	Asp	Cys	Ala	Gln	Asp	Val	Lys	Asn	Ile	Val	Asp	His	Leu	Lys	Ala
	340						345						350		
Ser	Gly	Arg	Ser	Glu	His	Lys	Met	His	Pro	Arg	Val	Tyr	Arg	Pro	Trp
	355						360						365		
Gly	Trp	Tyr	Glu	Gly	Ile	Asp	Ile	Gly	Glu	Arg	Phe	Gln	Val	Lys	Arg
	370					375						380			
Ile	Met	Val	Lys	Pro	Gly	Glu	Arg	Leu	Ser	Leu	Gln	Met	His	His	His
385				390						395				400	
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			405					410					415		
Asp	Asp	Val	Thr	Lys	Leu	Tyr	Thr	Glu	Asn	Glu	Ser	Thr	Tyr	Ile	Pro
	420							425					430		
Ile	Gly	Ser	Thr	His	Arg	Leu	Glu	Asn	Pro	Gly	Lys	Leu	Pro	Leu	His
	435					440						445			
Leu	Ile	Glu	Val	Gln	Ser	Gly	Ser	Tyr	Leu	Gly	Glu	Asp	Asp	Ile	Val
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Arg	Phe	Glu	Asp	Thr	Tyr	Gly	Arg	Ser							
465				470											

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<212> DNA

<213> Artificial Sequence

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<211> 33

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer MgtfA-R1

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<210> 7

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer Km4-F2

<400> 7

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<210> 8

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer Km4-R2

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<210> 9

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer Km4-R1

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<210> 10

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer mManC-F1

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<210> 11

<211> 28

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer mManC-R1

<400> 11

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<212> DNA

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<223> Description of Artificial Sequence: primer mManC-F2

<400> 12

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33

<210> 13

<211> 31

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer mManC-R2

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31